

ABSTRACT

[0100] Methods for classification of biological data including the use of mathematically based classification models are disclosed. In preferred embodiments, gene expression data derived from biological studies is used to classify events. The methods use a version of a linear discriminate model for deriving markers according to a technique whereby the model is limited to scoring the predictive ability of genes without making assumptions about inter-gene relationships, relative magnitudes or redundant information. In an associated method for building a fully informative database of biological information, biological studies are performed on a continual basis and linear discriminate models are used to provide rapid and efficient updates to gene markers.